

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/731,465
Source: IFW50
Date Processed by STIC: 10/14/04

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IFWO

RAW SEQUENCE LISTING

DATE: 10/14/2004

PATENT APPLICATION: US/10/731,465

TIME: 10:48:44

Input Set : D:\WhitsettReg.ST25 sequencing.txt

Output Set: N:\CRF4\10142004\J731465.raw

3 <110> APPLICANT: Whitsett, Jeffrey A.
 4 Glasser, Stephan W.
 6 <120> TITLE OF INVENTION: METHODS OF DIAGNOSIS AND TREATMENT OF INTERSTITIAL LUNG
 DISEASE
 8 <130> FILE REFERENCE: 0010872/0507287
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/731,465
 C--> 10 <141> CURRENT FILING DATE: 2003-12-09
 10 <150> PRIOR APPLICATION NUMBER: US 60/431,949
 11 <151> PRIOR FILING DATE: 2002-12-09
 13 <160> NUMBER OF SEQ ID NOS: 6
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 3633
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Mus musculus
 22 <300> PUBLICATION INFORMATION:
 23 <308> DATABASE ACCESSION NO: M38314
 24 <309> DATABASE ENTRY DATE: 1999-07-28
 25 <313> RELEVANT RESIDUES: (1)..(3633)
 28 <220> FEATURE:
 29 <221> NAME/KEY: gene
 30 <222> LOCATION: (321)..(3443)
 32 <220> FEATURE:
 33 <221> NAME/KEY: mRNA
 34 <222> LOCATION: (321)..(3443)
 35 <223> OTHER INFORMATION: join (321..389, 1619..1777, 2112..2234, 2472..2582,
 2911..3066,
 36 3268..3443)
 38 <220> FEATURE:
 39 <221> NAME/KEY: exon
 40 <222> LOCATION: (321)..(389)
 42 <220> FEATURE:
 43 <221> NAME/KEY: Intron
 44 <222> LOCATION: (390)..(1618)
 46 <220> FEATURE:
 47 <221> NAME/KEY: exon
 48 <222> LOCATION: (1619)..(1777)
 50 <220> FEATURE:
 51 <221> NAME/KEY: Intron
 52 <222> LOCATION: (1778)..(2111)
 54 <220> FEATURE:
 55 <221> NAME/KEY: exon
 56 <222> LOCATION: (2112)..(2234)
 58 <220> FEATURE:

59 <221> NAME/KEY: Intron

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60 <222> LOCATION: (2235)..(2471)
62 <220> FEATURE:
63 <221> NAME/KEY: exon
64 <222> LOCATION: (2472)..(2582)
66 <220> FEATURE:
67 <221> NAME/KEY: Intron
68 <222> LOCATION: (2583)..(2910)
70 <220> FEATURE:
71 <221> NAME/KEY: exon
72 <222> LOCATION: (2911)..(3066)
74 <220> FEATURE:
75 <221> NAME/KEY: Intron
76 <222> LOCATION: (3067)..(3267)
78 <220> FEATURE:
79 <221> NAME/KEY: exon
80 <222> LOCATION: (3268)..(3443)
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85 agcaggtggc ccgaggggtga gtttgcttga cctcaccag gtttgctctt gttggggcca      120
87 agaggattca tgtgcctagg ccaagggcct tgggggctct tgcagctgcc ttatcggggc      180
89 ctgggctctg aaaagccagg aacaaacaag ctacaaagcc aaggacttgg ctggcagaca      240
91 ggaggcccag tccttcaccc ctgtcctctc tgtctctgat gatatatata agacactggg      300
93 cacaccagag agatgaggag agg aga gag aga gag aaa cct tac aaa atg gac      353
94                               Arg Arg Glu Arg Glu Lys Pro Tyr Lys Met Asp
95                               1               5               10
97 atg agt agc aaa gag gtc ctg atg gag agt cca ccg gtgagtgtga      399
98 Met Ser Ser Lys Glu Val Leu Met Glu Ser Pro Pro
99                               15               20
101 ttgtgtgtgt gtgtgtgtgt gctgcgcgcg catacatagt atactgactt gactgtccat      459
103 cctccagtag gctttttttt tttttctaga cccatatact caattagctt aggattgggc      519
105 ttttaggata gagataccgt gatcattaag agtccctggg agaggcaggc acgacgacca      579
107 cgaattcctg tataaaggga ttgagagcca cagaggggtc aatagaaagt cctgtgaaga      639
109 aactgatag caccaccatg tagttgggag gctacaggaa gtaccacaga gcaaatgaca      699
111 gtgaggctgg gatgtagatc agtagctaga gcactttgca aaactgggag accctggggg      759
113 ttcagtcccc cagatccaca taatccaggc atagagggtg acactgtttg gaaatataag      819
115 caagataatc attcagggtc atccttagat atataaggag ttgaaaggca gcctgggtca      879
117 tagatatggg ttttttcttt aaaaaaaaaa aaaggatggc tcagtaggta gtgggtgcttg      939
119 caccaaagt ggcggtcga gtttaatctc tggaaattcac atgatgaaag gagatgaaaa      999
121 gttgtccctg acttacacac acacatgtac atacacactc acacatacta cacacatgta      1059
123 cacaacatt cacactcaca ccacatacac acactctcac acacaccaca cacatgtgca      1119
125 cacacacaca cacacatgta ccttcacaca catcacacac atgcacactc aaacatacca      1179
127 cacaatgtat acacgctcac acactaaatc cgtgtaaaaa accatgaagc tggcacatgg      1239
129 actggattga gaaggaacaa aggagaccgg tgtaaaggta tagagacagg gctacctgga      1299
131 tcctttgagg gagcaaaaac tcaggatatg tctgggggtg taggcgtcgt gggaaaacag      1359
133 aagaagagat cggtagctgg ctctcttgga ttatttcaaa cctagacttt gcttctaact      1419
135 ttctaagtag ctatggtttt gttagggtcc aaccaccttc cccaaagcct tccttcccaa      1479
137 aagcctctga tctccccagc tottcttca cactcgtagc cttaaagggt acgggatgtg      1539
139 tgtgtcccc ttgcacaggg agagtaggag ccacctctc cactaccac ttgtctctct      1599
141 gtttcccttg ctctctcag gat tac tcg gca ggt ccc agg agc cag ttc cgc      1651

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142          Asp Tyr Ser Ala Gly Pro Arg Ser Gln Phe Arg
143                25                30
145 atc ccc tgc tgt ccc gtg cac ctc aaa cgc ctt ctc atc gtg gtt gtg      1699
146 Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val Val Val
147 35                40                45                50
149 gtg gtg gtc ctc gtt gtc gtg gtg att gta ggg gct ctg ctc atg ggc      1747
150 Val Val Val Leu Val Val Val Val Ile Val Gly Ala Leu Leu Met Gly
151                55                60                65
153 ctc cac atg agt caa aaa cat act gag atg gtgagtgggc ctgggttggg      1797
154 Leu His Met Ser Gln Lys His Thr Glu Met
155                70                75
157 caaagaggca cagcagacag ggggttgggg gagattatgg gggatgggca gctgttcgga      1857
159 ggaagagaag ggagtggaca ggtatgagca catcttgggt gacacaaaca gagacgaggt      1917
161 agccatcctg cctagatcct ctccccagc cccggcctag tgtgataacc atcgattgct      1977
163 ctgacacctc ttacgtttag ccttcctgag atctcaggaa agcgtttgaa tagaggattc      2037
165 tgagtagata tgggtaccga aagctgaggg aagaaagaga aataccaggc agcattccaa      2097
167 cacccttccc ctag gtc ctt gag atg agc atc gga gca ccg gaa act cag      2147
168          Val Leu Glu Met Ser Ile Gly Ala Pro Glu Thr Gln
169                80                85
171 aaa cgc cta gcc ccg agt gag cga gca gac acc atc gct acc ttt tcc      2195
172 Lys Arg Leu Ala Pro Ser Glu Arg Ala Asp Thr Ile Ala Thr Phe Ser
173 90                95                100
175 atc ggc tcc act ggc atc gtt gtg tat gac tac cag cgg gtgaggatgc      2244
176 Ile Gly Ser Thr Gly Ile Val Val Tyr Asp Tyr Gln Arg
177 105                110                115
179 cggaggacca ccgggacttt attggaacta gccagttgta gcatttctag aggtctctcc      2304
181 ccattctgtg cctggctacc tcacctcaga tgctcgaacc actgacgcaa gtgcgccccct      2364
183 ccaccctctg aagacaatct aaaggaagtt ggttggctga gaactagggt tggggaggaa      2424
185 gcaaggcaag gggaccttgt gaatgacctc cagggtttta tacctag ctc ctg acg      2480
186          Leu Leu Thr
187                120
189 gcc tat aag cca gct cca gga acc tac tgc tac atc atg aag atg gct      2528
190 Ala Tyr Lys Pro Ala Pro Gly Thr Tyr Cys Tyr Ile Met Lys Met Ala
191                125                130                135
193 cca gag agc atc cct agt ctt gag gct ttc gct aga aaa ctc cag aac      2576
194 Pro Glu Ser Ile Pro Ser Leu Glu Ala Phe Ala Arg Lys Leu Gln Asn
195                140                145                150
197 ttc agg tgggtatggt tagggaggga gggagcagtc tcctctgagg tttgagtaga      2632
198 Phe Arg
201 agggacatgt gaaagatgac tagcgtaccc tgtgtagtat tgatgtttct gatcagacat      2692
203 gttctcctct ctccatgacc tgtgtcctgc catccctacc agctctcagg tggccctgct      2752
205 aagttgttgg ccttggctga gcttagacat gacctatggg cttctacatc caaccagtc      2812
207 cctctctgaa tttgtgagga aactgatoct cgagaattac caacttagtg tcccacacta      2872
209 aataaagcag gtgacattga aagtaggtgt tctttcca gcc aag ccc tcc aca ccc      2928
210          Ala Lys Pro Ser Thr Pro
211                155                160
213 acc tct aag ctg ggc cag gag gaa ggg cat gat act ggt tcc gag tcc      2976
214 Thr Ser Lys Leu Gly Gln Glu Glu Gly His Asp Thr Gly Ser Glu Ser
215                165                170                175

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217 gat tct tcc ggg aga gac ctg gct ttc cta ggc ctt gct gtg agc acc      3024
218 Asp Ser Ser Gly Arg Asp Leu Ala Phe Leu Gly Leu Ala Val Ser Thr
219          180          185          190
221 ctg tgt gga gag cta cca ctc tac tat atc tag cat cca cag      3066
222 Leu Cys Gly Glu Leu Pro Leu Tyr Tyr Ile      His Pro Gln
223          195          200          205
225 gtgagcaaca gtacctttca ggggtgcctgg gcaacactgg cagggccttgg gctgcctgct      3126
227 ttgtcagggg acctactagg tatctcttaa agtcagtggt ctcgaggagct cggaggatgg      3186
229 aggggttcca gacacatccc aactggacc caagcgggtg gcttcttcag tccccataag      3246
231 cattagttct ttgcttcaca g ggt cgg tag aaa ccg cag cgg gac agg aaa      3297
232          Gly Arg      Lys Pro Gln Arg Asp Arg Lys
233          210
235 gac cct ccg caa agg gtc ttt gtc aga caa gca gga agc tgc tcc tgc      3345
236 Asp Pro Pro Gln Arg Val Phe Val Arg Gln Ala Gly Ser Cys Ser Cys
237 215          220          225          230
239 cca gaa acc ggt gga agt ctg taa agg aaa ggt gtc tct cct acg ggc      3393
240 Pro Glu Thr Gly Gly Ser Leu      Arg Lys Gly Val Ser Pro Thr Gly
241          235          240          245
243 cag ggg gat cct atc aca aaa gaa taa agc agc ctg att gga aaa caa      3441
244 Gln Gly Asp Pro Ile Thr Lys Glu      Ser Ser Leu Ile Gly Lys Gln
245          250          255          260
247 ag agtggcgctt cttttctttc acattttctc agctcggtt ctagcagaag      3493
249 ctccctaggaa ggagagggtt tggagagttg ggcgctttgc acgtcctttc taagagtgat      3553
251 ggaggtttgg tctacccag gtaatgggaa cagagcaaaa ggcagggaca gaggacggga      3613
253 cctgggtgcc atacacgggg      3633
256 <210> SEQ ID NO: 2
257 <211> LENGTH: 995
258 <212> TYPE: DNA
259 <213> ORGANISM: Mus musculus
261 <400> SEQUENCE: 2
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264 agtccaccgg attactcggc aggtcccagg agccagttcc gcatcccttg ctgtcccgtg      120
266 cacctcaaac gccttctcat cgtgggttggt gtgggtgggtc tcgttgctgt ggtgattgta      180
268 ggggctctgc tcatgggcct ccacatgagt caaaaacata ctgagatggt ccttgagatg      240
270 agcatcggag caccggaaac tcagaaacgc ctagccccga gtgagcgagc agacaccatc      300
272 gctacctttt ccateggctc cactggcatc gttgtgtatg actaccagcg gctcctgacg      360
274 gcctataagc cagctccagg aacctactgc tacatcatga agatgggtcc agagagcatc      420
276 cctagtcttg aggttttcgc tagaaaactc cagaacttca gggccaagcc ctccacaccc      480
278 acctctaagc tgggccagga ggaaggcat gatactggtt ccgagtccga ttcttccggg      540
280 agagacctgg ctttcttagg ccttgctgtg agcaccctgt gtggagagct accactctac      600
282 tatatctagc atccacaggt gagcaacagt acctttcagg gtgcctgggc aacactggca      660
284 gggccttggg tgcctgcttt gtcaggggac ctactaggta tctcttaaag tcagtgtgtc      720
286 cgggagctcg gaggatggag ggttcccaga cacatccac actggacca agcgggtggc      780
288 ttcttcagtc cccataagca ttagttcttt gcttcacagg gtcggtagaa accgcagcgg      840
290 gacaggaaag accctccgca aagggtcttt gtcagacaag caggaagctg ctctgcccc      900
292 gaaaccggtg gaagtctgta aaggaaaggt gtctctccta cgggccaggg ggatcctatc      960
294 acaaaagaat aaagcagcct gattggaaaa caaag      995
297 <210> SEQ ID NO: 3
298 <211> LENGTH: 193

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TIME: 10:48:45

Input Set : D:\WhitsettReg.ST25 sequencing.txt

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299 <212> TYPE: PRT
300 <213> ORGANISM: Mus musculus
302 <300> PUBLICATION INFORMATION:
303 <308> DATABASE ACCESSION NO: AAA40010
304 <309> DATABASE ENTRY DATE: 1999-07-28
305 <313> RELEVANT RESIDUES: (1)..(193)
307 <400> SEQUENCE: 3
309 Met Asp Met Ser Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
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313 Ser Ala Gly Pro Arg Ser Gln Phe Arg Ile Pro Cys Cys Pro Val His
314 20 25 30
317 Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Val Val Val
318 35 40 45
321 Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His
322 50 55 60
325 Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Thr Gln Lys
326 65 70 75 80
329 Arg Leu Ala Pro Ser Glu Arg Ala Asp Thr Ile Ala Thr Phe Ser Ile
330 85 90 95
333 Gly Ser Thr Gly Ile Val Val Tyr Asp Tyr Gln Arg Leu Leu Thr Ala
334 100 105 110
337 Tyr Lys Pro Ala Pro Gly Thr Tyr Cys Tyr Ile Met Lys Met Ala Pro
338 115 120 125
341 Glu Ser Ile Pro Ser Leu Glu Ala Phe Ala Arg Lys Leu Gln Asn Phe
342 130 135 140
345 Arg Ala Lys Pro Ser Thr Pro Thr Ser Lys Leu Gly Gln Glu Glu Gly
346 145 150 155 160
349 His Asp Thr Gly Ser Glu Ser Asp Ser Ser Gly Arg Asp Leu Ala Phe
350 165 170 175
353 Leu Gly Leu Ala Val Ser Thr Leu Cys Gly Glu Leu Pro Leu Tyr Tyr
354 180 185 190
357 Ile
361 <210> SEQ ID NO: 4
362 <211> LENGTH: 3409
363 <212> TYPE: DNA
364 <213> ORGANISM: Homo sapiens
366 <300> PUBLICATION INFORMATION:
367 <308> DATABASE ACCESSION NO: J03890
368 <309> DATABASE ENTRY DATE: 1998-08-17
369 <313> RELEVANT RESIDUES: (1)..(3409)
372 <220> FEATURE:
373 <221> NAME/KEY: gene
374 <222> LOCATION: (591)..(3237)
376 <220> FEATURE:
377 <221> NAME/KEY: mRNA
378 <222> LOCATION: (591)..(3237)
379 <223> OTHER INFORMATION: join(616..657,1356..1514,1860..1982,2206..2316,2651..2809);
380 gene="SP-C1"; product="pulmonary surfactant protein SP-C"
382 <220> FEATURE:

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:505 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4